AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

Claims 1- 20 (cancelled)

21. (previously presented) A method of genotyping comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of said first subpopulation comprise at least first and second different target nucleic acid molecules from a first individual and the microspheres of said second subpopulation comprise at least first and second different target nucleic acid molecules from a second individual, wherein said at least first and second different target nucleic acid molecules are covalently attached to each of said microspheres with first and second attachment moieties, respectively;

wherein said microspheres are randomly distributed on said surface;

b) contacting said array composition with a first set of extension probes that hybridize with at least said first target nucleic acid molecules adjacent to a first detection position to form an extension complex;

c) contacting said extension complex with a composition comprising

i) at least a first nucleotide;

ii) polymerase;

wherein said polymerase extends a first extension probe with said first nucleotide when said first nucleotide is complementary to said first detection position; and

d) detecting the presence of said first nucleotide, whereby said genotype is determined.

22. (original) The method according to claim 21, wherein said first nucleotide comprises a label.

Claim 23 (cancelled)

24. (currently amended) ~~The method according to claim 23,~~ A method of determining the identification of a nucleotide at a detection position in at least a first target nucleic acid molecule comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of said first subpopulation comprise a plurality of different target nucleic acid molecules from a first individual and the microspheres of said second subpopulation comprise a plurality of different target nucleic acid molecules from a second individual, and wherein a plurality of said different target nucleic acid molecules are covalently attached to each of said microspheres, wherein said microspheres are distributed on said surface;

b) forming a first hybridization complex between said first target nucleic acid molecule and at least a first readout probe, wherein said first target nucleic acid molecule comprises a first and a second target domain, wherein said first hybridization complex comprises said first target nucleic acid molecule, a first readout probe hybridized to said first domain and a second readout probe hybridized to said second domain, wherein at least one of said readout probes comprise a label said determining comprises adding a ligase to form a ligation complex, and

c) determining the nucleotide at said detection position.

Claim 25 (cancelled)

26. (currently amended) ~~The method according to claim 23, further comprising~~ A method of determining the identification of a nucleotide at a detection position in at least a first target nucleic acid molecule comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of said first subpopulation comprise a plurality

of different target nucleic acid molecules from a first individual and the microspheres of said second subpopulation comprise a plurality of different target nucleic acid molecules from a second individual, and wherein a plurality of said different target nucleic acid molecules are covalently attached to each of said microspheres, wherein said microspheres are distributed on said surface;

b) forming a first hybridization complex between said first target nucleic acid molecule and at least a first readout probe;

c) contacting said hybridization complex with at least a first nucleotide and a polymerase, wherein said polymerase extends said first readout probe with said first nucleotide when said first nucleotide is complementary to said first detection position, and

d) determining the nucleotide at said detection position.

27. (currently amended) The method according to claims ~~14,~~ 21, 24 or 26 ~~or 23~~ wherein said substrate is a fiber optic bundle.

28. (currently amended) The method according to claim s ~~14,~~ 21, 24 or 26 ~~or 23~~ wherein said substrate is selected from the group consisting of glass and plastic.

29. (previously presented) The method according to claim s ~~14,~~ 21, 24 or 26 ~~or 23~~ further comprising contacting said microspheres with decoder binding ligands, wherein the microspheres of each subpopulation comprises an identifier binding ligand that will bind a decoder binding ligand for identification and elucidation of said target analyte.

Claims 30-35 (cancelled)

36. (previously presented) A method of genotyping comprising:

a) providing an array composition comprising:

i) a substrate with a surface comprising discrete sites; and

ii) a population of microspheres comprising at least a first and a second subpopulation, wherein the microspheres of said first subpopulation comprise at least first and second different target nucleic acid molecules from a first individual and the microspheres of said second subpopulation comprise at least first and second different target nucleic acid molecules from a second individual, wherein said plurality of first and

second different target nucleic acid molecules are attached to each of said microspheres via receptor-ligand interaction; wherein said target analytes are derivatized with said receptor or said ligand,

wherein said microspheres are randomly distributed on said surface;

b) contacting said array composition with a first set of extension probes that hybridize with at least said first target nucleic acid molecule adjacent to a first detection position to form an extension complex;

c) contacting said extension complex with a composition comprising

i) at least a first nucleotide;

ii) polymerase;

wherein said polymerase extends a first extension probe with said first nucleotide when said first nucleotide is complementary to said first detection position; and

d) detecting the presence of said first nucleotide, whereby said genotype is determined.

Claim 37 (cancelled)

38. (currently amended) The method according to claim ~~35, 36 or 37~~, wherein said receptor is streptavidin and said ligand is biotin.

39. (previously presented) The method according to claim 38, wherein said microspheres are streptavidin coated.